

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5
- (i) APPLICANT: Jacobs, Cindy A.
- (ii) TITLE OF INVENTION: Method of Treating TNF-Dependent Inflammation
Using Tumor Necrosis Factor Antagonists
- 10
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
- 15
- (A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: U.S.A.
(F) ZIP: 98101
- 20
- (v) COMPUTER READABLE FORM:
- 25
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- 30
- (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- 35
- (A) NAME: Wight, Christopher L.
(B) REGISTRATION NUMBER: 31,680
(C) REFERENCE/DOCKET NUMBER: 2503
- (ix) TELECOMMUNICATION INFORMATION:
- 40
- (A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 587-0606

(2) INFORMATION FOR SEQ ID NO:1:

- 45
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 50
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- 55
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
(G) CELL TYPE: Fibroblast
(H) CELL LINE: WI-26 VA4
- 60
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: WI-26 VA4
(B) CLONE: Clone 1
- 65

25
26

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 88..1473

5 (ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 154..1470

10 (ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 88..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 GCGAGGCAGG CAGCCTGGAG AGAAGGCGCT GGGCTGCGAG GGC GCGAGGG CGCGAGGGCA 60
GGGGGCAACC GGACCCCGCC CGCATCC ATG GCG CCC GTC GCC GTC TGG GCC 111
Met Ala Pro Val Ala Val Trp Ala
20 -22 -20 -15
GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC 159
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
-10 -5 1
25 GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC 207
Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
5 10 15
30 CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA 255
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
20 25 30
35 TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC 303
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
35 40 45 50
40 ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC 351
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
55 60 65
TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG 399
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
70 75 80
45 GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC 447
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
85 90 95
50 AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG 495
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu
100 105 110
55 TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA 543
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro
115 120 125 130
GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG GGG ACG 591
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
135 140 145
60 TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC CAG ATC 639
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile
150 155 160
65

	TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	687
	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
			165					170					175				
5	ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	735
	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
		180					185					190					
10	CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	783
	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
		195				200					205					210	
15	CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	831
	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
					215					220					225		
20	CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	879
	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
				230					235					240			
25	ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	927
	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
			245					250						255			
30	TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	975
	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
		260					265					270					
35	GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	1023
	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
		275				280					285					290	
40	GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC	1071
	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	
					295					300					305		
45	AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT	1119
	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	
				310						315				320			
50	CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG	1167
	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	
			325					330					335				
55	GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG	1215
	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	
			340				345					350					
60	ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC	1263
	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	
						360					365					370	
65	CAC	AGC	TCA	CAG	TGC	TCC	TCC	CAA	GCC	AGC	TCC	ACA	ATG	GGA	GAC	ACA	1311
	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	
					375					380					385		
70	GAT	TCC	AGC	CCC	TCG	GAG	TCC	CCG	AAG	GAC	GAG	CAG	GTC	CCC	TTC	TCC	1359
	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	
				390					395					400			
75	AAG	GAG	GAA	TGT	GCC	TTT	CGG	TCA	CAG	CTG	GAG	ACG	CCA	GAG	ACC	CTG	1407
	Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	
			405					410					415				

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27

CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT	1455
Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala	
420 425 430	

5	GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGGCT GTGTCGTAGC CAAGGTGGGC	1510
	Gly Met Lys Pro Ser	
	435 440	

10	TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG	1570
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	GACTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT	1630
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	CTGACCTGCA G	1641
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15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 461 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
-22 -20 -15 -10

30

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
-5 1 5 10

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
15 20 25

35

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
30 35 40

40

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
45 50 55

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
60 65 70

45

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
75 80 85 90

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
95 100 105

50

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
110 115 120

55

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
125 130 135

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
140 145 150

60

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
155 160 165 170

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
175 180 185

65

28

	Met	Ala	Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	
				190					195					200			
5	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	
			205					210					215				
	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	
		220					225					230					
10	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	
		235				240					245					250	
	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	
				255						260					265		
15	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	
			270						275					280			
20	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	
		285						290					295				
	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	
		300					305					310					
25	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	
		315				320					325					330	
	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	
				335						340					345		
30	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	
			350						355					360			
35	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	
		365						370					375				
	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	
		380					385					390					
40	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	
		395				400					405					410	
	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	Leu	Gly	Ser	Thr	Glu	Glu	Lys	Pro	
				415						420					425		
45	Leu	Pro	Leu	Gly	Val	Pro	Asp	Ala	Gly	Met	Lys	Pro	Ser				
			430						435								

50 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1557 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

60 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vii) IMMEDIATE SOURCE:

(B) CLONE: TNFR/Fc Fusion Protein

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1557

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..1554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15	GCG AGG CAG GCA GCC TGG AGA GAA GGC GCT GGG CTG CGA GGG CGC GAG	48
	Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu	
	1 5 10 15	
20	GGC GCG AGG GCA GGG GGC AAC CGG ACC CCG CCC GCA TCC ATG GCG CCC	96
	Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro	
	20 25 30	
25	GTC GCC GTC TGG GCC GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG	144
	Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala	
	35 40 45	
30	GCG CAC GCC TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG	192
	Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu	
	50 55 60	
35	CCC GGG AGC ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG	240
	Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln	
	65 70 75 80	
40	ATG TGC TGC AGC AAA TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT	288
	Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys	
	85 90 95	
45	ACC AAG ACC TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC	336
	Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr	
	100 105 110	
50	ACC CAG CTC TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC	384
	Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg	
	115 120 125	
55	TGT AGC TCT GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC	432
	Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn	
	130 135 140	
60	CGC ATC TGC ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG	480
	Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln	
	145 150 155 160	
65	GAG GGG TGC CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC	528
	Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe	
	165 170 175	
70	GGC GTG GCC AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC	576
	Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro	
	180 185 190	
75	TGT GCC CCG GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC	624
	Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys	
	195 200 205	

5	AGG Arg 210	CCC Pro 210	CAC His 210	CAG Gln 210	ATC Ile 210	TGT Cys 215	AAC Asn 215	GTG Val 215	GTG Val 215	GCC Ala 215	ATC Ile 220	CCT Pro 220	GGG Gly 220	AAT Asn 220	GCA Ala 220	AGC Ser 220	672
10	ATG Met 225	GAT Asp 225	GCA Ala 225	GTC Val 225	TGC Cys 230	ACG Thr 230	TCC Ser 230	ACG Thr 230	TCC Ser 230	CCC Pro 235	ACC Thr 235	CGG Arg 235	AGT Ser 235	ATG Met 240	GCC Ala 240	CCA Pro 240	720
15	GGG Gly 245	GCA Ala 245	GTA Val 245	CAC His 245	TTA Leu 245	CCC Pro 245	CAG Gln 245	CCA Pro 245	GTG Val 250	TCC Ser 250	ACA Thr 250	CGA Arg 250	TCC Ser 255	CAA Gln 255	CAC His 255	ACG Thr 255	768
20	CAG Gln 260	CCA Pro 260	ACT Thr 260	CCA Pro 260	GAA Glu 260	CCC Pro 260	AGC Ser 265	ACT Thr 265	GCT Ala 265	CCA Pro 265	AGC Ser 265	ACC Thr 265	TCC Ser 270	TTC Phe 270	CTG Leu 270	CTC Leu 270	816
25	CCA Pro 275	ATG Met 275	GGC Gly 275	CCC Pro 275	AGC Ser 275	CCC Pro 275	CCA Pro 280	GCT Ala 280	GAA Glu 280	GGG Gly 280	AGC Ser 285	ACT Thr 285	GGC Gly 285	GAC Asp 285	GAG Glu 285	CCC Pro 285	864
30	AAA Lys 290	TCT Ser 290	TGT Cys 290	GAC Asp 290	AAA Lys 295	ACT Thr 295	CAC His 295	ACA Thr 295	TGC Cys 295	CCA Pro 295	CCG Pro 295	TGC Cys 300	CCA Pro 300	GCA Ala 300	CCT Pro 300	GAA Glu 300	912
35	CTC Leu 305	CTG Leu 305	GGG Gly 305	GGA Gly 305	CCG Pro 310	TCA Ser 310	GTC Val 310	TTC Phe 310	CTC Leu 310	TTC Phe 315	CCC Pro 315	CCA Pro 315	AAA Lys 315	CCC Pro 315	AAG Lys 315	GAC Asp 320	960
40	ACC Thr 325	CTC Leu 325	ATG Met 325	ATC Ile 325	TCC Ser 325	CGG Arg 325	ACC Thr 325	CCT Pro 325	GAG Glu 330	GTC Val 330	ACA Thr 330	TGC Cys 330	GTG Val 335	GTG Val 335	GTG Val 335	GAC Asp 335	1008
45	GTG Val 340	AGC Ser 340	CAC His 340	GAA Glu 340	GAC Asp 340	CCT Pro 340	GAG Glu 345	GTC Val 345	AAG Lys 345	TTC Phe 345	AAC Asn 345	TGG Trp 345	TAC Tyr 350	GTG Val 350	GAC Asp 350	GGC Gly 350	1056
50	GTG Val 355	GAG Glu 355	GTG Val 355	CAT His 355	AAT Asn 355	GCC Ala 355	AAG Lys 360	ACA Thr 360	AAG Lys 360	CCG Pro 360	CGG Arg 360	GAG Glu 365	GAG Glu 365	CAG Gln 365	TAC Tyr 365	AAC Asn 365	1104
55	AGC Ser 370	ACG Thr 370	TAC Tyr 370	CGG Arg 370	GTG Val 375	GTC Val 375	AGC Ser 375	GTC Val 375	CTC Leu 375	ACC Thr 375	GTC Val 375	CTG Leu 380	CAC His 380	CAG Gln 380	GAC Asp 380	TGG Trp 380	1152
60	CTG Leu 385	AAT Asn 385	GGC Gly 385	AAG Lys 385	GAC Asp 390	TAC Tyr 390	AAG Lys 390	TGC Cys 390	AAG Lys 390	GTC Val 395	TCC Ser 395	AAC Asn 395	AAA Lys 395	GCC Ala 395	CTC Leu 400	CCA Pro 400	1200
65	GCC Ala 405	CCC Pro 405	ATG Met 405	CAG Gln 405	AAA Lys 405	ACC Thr 405	ATC Ile 405	TCC Ser 410	AAA Lys 410	GCC Ala 410	AAA Lys 410	GGG Gly 415	CAG Gln 415	CCC Pro 415	CGA Arg 415	GAA Glu 415	1248
70	CCA Pro 420	CAG Gln 420	GTG Val 420	TAC Tyr 420	ACC Thr 420	CTG Leu 420	CCC Pro 425	CCA Pro 425	TCC Ser 425	CGG Arg 425	GAT Asp 425	GAG Glu 430	CTG Leu 430	ACC Thr 430	AAG Lys 430	AAC Asn 430	1296
75	CAG Gln 435	GTC Val 435	AGC Ser 435	CTG Leu 435	ACC Thr 435	TGC Cys 440	CTG Leu 440	GTC Val 440	AAA Lys 440	GGC Gly 440	TTC Phe 440	TAT Tyr 445	CCC Pro 445	AGG Arg 445	CAC His 445	ATC Ile 445	1344
80	GCC Ala 450	GTG Val 450	GAG Glu 450	TGG Trp 450	GAG Glu 455	AGC Ser 455	AAT Asn 455	GGG Gly 455	CAG Gln 455	CCG Pro 455	GAG Glu 460	AAC Asn 460	AAC Asn 460	TAC Tyr 460	AAG Lys 460	ACC Thr 460	1392

	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	1440
	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	
	465					470					475					480	
5	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	1488
	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	
					485					490					495		
10	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	1536
	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	
				500					505					510			
15	TCC	CTG	TCT	CCG	GGT	AAA	TGA										1557
	Ser	Leu	Ser	Pro	Gly	Lys											
			515														

(2) INFORMATION FOR SEQ ID NO:4:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30	Ala	Arg	Gln	Ala	Ala	Trp	Arg	Glu	Gly	Ala	Gly	Leu	Arg	Gly	Arg	Glu
	1				5					10					15	
	Gly	Ala	Arg	Ala	Gly	Gly	Asn	Arg	Thr	Pro	Pro	Ala	Ser	Met	Ala	Pro
		20						25					30			
35	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu	Leu	Trp	Ala	Ala
		35					40						45			
	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu
40		50					55					60				
	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln
	65					70				75						80
45	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys
					85					90					95	
	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr
				100					105					110		
50	Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg
		115						120					125			
	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn
55		130					135					140				
	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln
	145					150				155						160
60	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe
					165					170					175	
	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro
				180					185					190		

	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	
			195					200					205				
5	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	
		210					215					220					
	Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	
	225					230					235					240	
10	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	
					245					250					255		
	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	
				260					265					270			
15	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Glu	Pro	
			275					280					285				
20	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
		290					295					300					
	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
	305					310					315					320	
25	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
					325					330							
	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
				340					345					350			
30	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	
			355					360					365				
35	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
		370					375					380					
	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	
	385					390					395					400	
40	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	
					405					410					415		
	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	
				420					425					430			
45	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	
			435					440					445				
50	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	
		450					455					460					
	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	
	465					470					475					480	
55	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	
					485					490					495		
	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	
				500					505					510			
60	Ser	Leu	Ser	Pro	Gly	Lys											

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(vii) IMMEDIATE SOURCE:

(B) CLONE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTACGTGC TGTTGTTACT GC

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